Target ID | GO.6042
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Source Organism | Arabidopsis thaliana
Target Name | At1g77540.1
PDB Entry | 2EVN (replaced 1XO4) Deposition: 5-Oct-2004
BMRB Entry | 6338 Deposition: 5-Oct-2004
Function | putative acetyltransferase (FF/Refine: 2IL4 [REPLACED 2GDB], 2Q4Y)
Produced From | E. coli B834(DE3)/pLacIRARE
Structure by NMR | Restraints/Residue: 19 Subunits/Molecule: 1
| No. of Residues: 103 Molecular Weight: 11.7 kDa
| Backbone RMSD(7−87): 0.48 Å All Heavy Atoms RMSD(7−87): 0.86 Å
Data Collected At | Nuclear Magnetic Resonance Facility at Madison (NMRFAM)
Authors | R.C. Tyler, S. Singh, M.S. Lee, J.L. Markley

Structural Features

The most similar structure in the PDB was GCN5-like putative N-acetyltransferase from Staphylococcus aureus (1R57) with 32% sequence identity over 71 residues. Several other targets with similar fold were co-crystallized with acetyl coenzyme A or coenzyme A with or without putative substrate. In view of these findings, the titration of ^15^N-At1g77540.1 with coenzyme A was followed by NMR spectroscopy. The ^1^H-^15^N HSQC chemical shift perturbation clearly demonstrated the binding and the location of this ligand. The coenzyme A binding site was mapped to At1g77540.1 residues in the cavity formed by C-terminal residue of β-sheet 4 (β4), loop residues spanning β4 and the N-terminal central helix (α1), N-terminal residues of α1 and residues of smaller perpendicularly oriented helix (α-2) in agreement with the X-ray co-crystal structures. Thus, it is most likely that At1g77540.1 functions as acetyl transferase. This target aligns to two Pfam domains of Pfam-B_34288 over residues 2−29 and Pfam-B_2135 over residues 30−79.


Percent Identity with Nearest PDB Structure at Time Solved | 32% over 71 aa (1R57)
Pfam Cluster | B_34288, B_2135
Protonet Cluster Size : Structures in PDB | 22 : 0

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